IN THE CLAIMS

The following is a copy of Applicant's claims that identifies language being added with underlining ("___") and language being deleted with strikethrough ("—"), as is applicable:

1. (Currently amended) A method of performing nanopore data analysis with a nanopore device, comprising:

providing a sample including target ~~polymers~~ polynucleotides and non-target ~~polymers~~ polynucleotides ~~and a nanopore device, wherein the target polymers and non-target polymers are selected from polynucleotides and polypeptides~~;

introducing the sample to the nanopore device;

generating nanopore data points corresponding to each target ~~polymer~~ polynucleotide and each non-target ~~polymer~~ polynucleotide traversing an aperture of the nanopore;

forming a distribution pattern of the nanopore data points; and

analyzing a distribution of ~~polymer~~ polynucleotide data points in the distribution pattern to aid in a determination of at least one of the following: phosphorylation state of the target polynucleotides, length diversity among polynucleotides present in a sample, chemical integrity of the target polynucleotides, and a ratio of target polynucleotides to non-target polynucleotides in the sample.

2. (Original) The method of claim 1, wherein the distribution pattern includes at least one data cluster, and wherein analyzing includes analyzing the distribution of target polynucleotide data points within the at least one data cluster.

3. (Original) The method of claim 2, further comprising:

comparing the distribution of the target polynucleotide data points between two data clusters to a phosphorylation state standard distribution.

4. (Original) The method of claim 3, further comprising:

determining a ratio of phosphorylated target polynucleotide to non-phosphorylated target polynucleotides.

5. (Currently amended) The method of claim 2, wherein the target polynucleotides comprise phosphorylated and non-phosphorylated polynucleotides, the method further comprising:

determining a ratio of phosphorylated target polynucleotide to non-phosphorylated target polynucleotides.

6. (Original) The method of claim 2, further comprising:

comparing a density distribution of the target polynucleotide data points to a chemical integrity standard density distribution, wherein a change in the density distribution of target polynucleotide data points as compared to the chemical integrity standard density distribution indicates that the chemical integrity of the target polynucleotides in the sample is different than a chemical integrity for which the chemical integrity standard density distribution was prepared.

7. (Original) The method of claim 6, further comprising:

determining the density of target polynucleotide data points in a defined area; and

comparing the density of the target polynucleotide data points to a chemical integrity standard density distribution for the defined area.

8. (Original) The method of claim 6, further comprising:

determining the density of target polynucleotide data points in a defined area;

comparing the density of the target polynucleotide data points to a density of the target polynucleotide data points of at least two other samples including target polynucleotides and non-target polynucleotides; and

ranking the samples based on the density of the target polynucleotide data points.

9. (Original) The method of claim 6, further comprising:

determining a cluster score for the target polynucleotide data points in a defined area; and

comparing the cluster score for the target polynucleotide data points to a cluster score for a chemical integrity standard density distribution for the defined area.

10. (Original) The method of claim 2, further comprising:

analyzing the distribution of the non-target polynucleotide data points.

11. (Original) The method of claim 10, wherein distribution of non-target polynucleotide data points outside of the at least one cluster indicates that non-target polynucleotides have a different length than the target polynucleotides.

12. (Original) The method of claim 10, wherein distribution of non-target polynucleotide data points outside of the at least one cluster indicates that the non-target polynucleotides have the same length as the target polynucleotide but the sequence of the non-target polynucleotide and target polynucleotide is not the same.

13. (Original) The method of claim 10, further comprising:

determining a ratio between the target polynucleotide data points and the non-target polynucleotide data points.

14. (Currently amended) The method of claim 1, wherein the failure of ~~polymer~~ polynucleotide data points to form at least one cluster indicates that the target ~~polymers~~ polynucleotides in the sample represent less than a calibration specified fraction of the total ~~polymers~~ polynucleotides in the sample.

15. (Currently amended) A system for performing nanopore data analysis, comprising:

a nanopore system including a nanopore device and a nanopore data analysis system, the nanopore device having a structure having an aperture, the nanopore data analysis system operative to:

generate nanopore data points corresponding to each target ~~polymer~~ polynucleotide and each non-target ~~polymer~~ polynucleotide traversing the aperture of the nanopore structure;

form a distribution pattern of the data points; and

analyze a distribution of target ~~polymer~~ polynucleotide data points in the distribution pattern to aid in a determination of at least one of the following: phosphorylation state of the target polynucleotides, length diversity among polynucleotides present in a sample, chemical integrity of the target polynucleotides, and a ratio of target polynucleotides to non-target polynucleotides in the sample.

16. (Currently amended) The system of claim 15, wherein the nanopore data analysis system is further operative to analyze the distribution of the non-target ~~polymer~~ polynucleotide data points.

17. (Currently amended) The system of claim 16, wherein the nanopore data analysis system is further operative to determine a ratio between the target ~~polymer~~ polynucleotide data points and the non-target ~~polymer~~ polynucleotide data points.

18. (Currently amended) The system of claim 15, wherein the distribution pattern includes at least one data cluster and wherein the nanopore data analysis system is further operative to:

analyze of the distribution of target ~~polymer~~ polynucleotide data points between the two data clusters;

~~comparing~~ compare the distribution of the target ~~polymer~~ polynucleotide data points between the two data clusters to a phosphorylation state standard distribution; and

determine a ratio of phosphorylated target ~~polymer~~ polynucleotide to non-phosphorylated target ~~polymers~~ polynucleotides.

19. (Currently amended) The system of claim 15, wherein the nanopore data analysis system is further operative to:

determine a cluster score for the target ~~polymer~~ polynucleotide data points in a defined area; and

compare the cluster score for the target ~~polymer~~ polynucleotide data points to a cluster score for a chemical integrity standard density distribution for the defined area in a distribution of a target ~~polymer~~ polynucleotide standard.

20. (Original) The system of claim 15, wherein the nanopore data analysis system is stored on a computer-readable medium.

21. (Currently amended) The system of claim 15, further comprising:

means for analyzing the distribution of target ~~polymer~~ polynucleotide data points in the distribution pattern.